

[illegible]

Figure 3

10 20 30 40 50 60 70 80 90 100 110 120
GAATTCATCGTGGCAAGGGCAGCCTGAATGGATGATGTAACCTGGGGTCTCTTCAATGGAGGGCCAGACTCCTGGGTCTAGGGGATGAGGGAGGGGAGGATCGGGTTAGCTGGGACCCA

130 140 150 160 170 180 190 200 210 220 230 240
GGTGAAGGGGCTGGGGGCCACATTCTGAGTCTCAGAGAGAAGGATCTGGGGTCTCAAGCACCTGAGTCGGAGGGAGGAGGGGTCTGGGCTCCTGAAAAACCACCTCTTGGACCAT

250 260 270 280 290 300 310 320 330 340 350 360
CTATGCAGATCACGCAGAACAGAGAAATTTCTGCGCCCATCTGAATTTCTAAGTTTGGGGGAGGGCGTGATCTGACACTGAGGTTCTTGATCCTCAGCAAGCGGCAATTGCTGTA

370 380 390 400 410 420 430 440 450 460 470 480
TGAAGAAGCGACCGCATCTGAGACACAAGTATCCTGCCTTGAAGCCTCTCACCTGGCCGTGGGCCAACCTCAACCTCATCTGTCCTGCTCAGATGCTCAGACCCTGGACATCCAGC

490 500 510 520 530 540 550 560 570 580 590 600
CTCCTCCTCCTGATGCAATCCTGGTGTCTTTTACCAGAGAAGCCATCCCAGGCCCAGGCAGGTGCTCCTGAAATAACCTGGGGGAGGGGTGGCTGAAAGTCCCTGACTGGAGTTGG

610 620 630 640 650 660 670 680 690 700 710 720
CAGCCAAGCCAGGCCCTGGAGTGGGCACCCAGAGGGAAGACAGGTGGCTAATTTCTTGGAGCCCCAAGGGTGAAGGGTAGGCCCTTCTGTGTCTGAGGGAGGAGGGGTGGGGCTCTGG

730 740 750 760 770 780 790 800 810 820 830 840
ACTCCTGGGTCTGAGGGAGGAGGGGTGGGGGCCCTGACTCCTGGGTCTGAGGGAGGAGGGTCTGGGCCTGTAACCTGGATCTGAGGGAGGAGGGGTGGGAACTTGGGCTCCTGGGT

850 860 870 880 890 900 910 920 930 940 950 960
CTGAGGGAGGAGGGAGCTTTGGTCTGGAATCCTGGGTCTGAGGGAGTAGGGCTAGGGATCTGGAATCTGGGTGTGAGGAAGGAGGGGTGGGGTCTGGAATCCTGGGTCTGAGGAAG

970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080
GAGGGGAGGGGGCTTGGACTCCTGGGTCTGAGGAAGGAGGGGCCGGGAGCCTGGACTCCTAAGTCTGAGGGAGGAGGGTCTGGGGCCTGGACTGCTGGGTGTGAGCAGAAGGGTCTGG

1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
GTGCTGGGAGTCCCAGCCTGGGGAGATGATGGTTAACTTCTGGGAATCAAGTCAAACCTCCTGAGTCTTTGACATTGATGTATCTTGAATGGGAGGGTCAGTCTGTGGGAAGGATTAC

1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320
CCAGGTGCCGAGGCAAGAGACTGAAGGCACAACTGTTTCAGTATAATAAGAAAAATAGTTAGAATAAGAAATAGTTATCATACAAATTAGATATAGAGATGATCATGGACAGTATCAATC

1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440
ATTAGTGTAACATTATTAATCATTAGCTATTACTTTTATTCTTTGTTGTATAACTAATATAACCAGGAAACAACCGGTGGGTATAGGGTCAGGTAAGAGGGACATTGTGAGAAGTGA

1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
CCTAGAAGGCAAGAGGTGAGCCTTCTGTACACCGGCATAAGGGCCTCTTGAGGGCTCCTTGGTCAAGCGGGAACGCCAGTGTCTGGGAAGGCACCCGTTACTCAGCAGACCACGAAAGG

1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680
GAATCTCCTTTCTTGGAGGAGTCAGGGAACACTCTGCTCCACGAGCTTCTTGTGGGAGGCTGGGTATTATCTAGGCCTGCCCGCAGTCATCCTGCTGTGCTGTCTTCAATGGTCACGC

1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800
TCCTTGCTCCTTGCATTTCTCCCGTACTCCTGGTCTCTTTGAAGTTCGTAGTAGATAGCGGTAGAAGAAATAGTGAAGCCTTTTTTTTTTTTTTTTGGGGGAGTCTCGCTC

Figure 3 (cont'd)

Sequence III (cont.)

1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920
TGCCCCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAATCTCCGCCTCCTGGGTTACACCATTTCTCCTGCCTCACCTCCCAAATAGCTAGGACTACAGGCGCCCTCCACC

1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040
ACGCGCCCGGATAATTTTTTGTATTTTAGTAGAGACAGGGTTTACCGTGTTAGCCAGGATGGCCTCCACCTCCTGACCTTGTGATCCGCCCCGCTCAGCCTCCCAAAGTGGTGGGATT

2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160
ACAGGCGTGAGCCACCGCGCCCGCCGAAATAGTGAAAGTCTTAAAGTCTTTGATCTTTCTTATAAGTGACAGAGAAGAAACGCTGACATATGCTGCCTTCTTTCTGCTTCGGCTGCC

2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280
TAAAGGGAAGGGCCCCCTGTCCCATGATCAGTGACTTGCTTGACCTTATCAGTCATTTGGACGACTCACCTCCTTATCCTGCCCCCCCTTGTCTTGATACAATAAATATCAGCGCG

2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400
CCCAGCCATTTCGGGGCCACTACCGGTCTCTCGCTTGTGATGGTAGTGGTCCCCCGGGGCCAGCTGTTTTCTCTTTATCTCTTTGTCTTTGTCTTTATTTCTTACAATCTCTCCTCTCCT

2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520
CACAGGGGAAGAACACCCACCCGAAAGCCCGTAGGGCTGGACCTACGTTAGCCTGCCCTGCTCGGGGTTGGCGATGCTGGAGGTGGGCCTTGGACCAGAGAAATGCTTTAATTAGG

2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640
TGACAAAGCGGGCAGAGGCCCTTTGTCTCTGGCGCCGGCAGCCACGGCCCCCGCTGACGGCGTGGGAAACAGACCCTGTTCCACTCCGGTCTCCAGCCTTGGAAATGGTTGCCTTCGTGCGAT

2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760
GCAGGTCTGGAAGTAGCAGTTTGGCACGGGACCTAGAAATCCCCAAAAGGAGTGACTAGGGGCTGGGATTCTGGAATTTGAGTGTGGACGGTGAGGCGGGGGGTGTGGGAGATCGGAG

2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880
ACCCTGGTGGGCGGGGAGCACCTGCAGGCTGGAGGCCCTCGCGCGTCCGGCGGACGCTGGCAAACAGGTCTCCATCCCCAGGAGGACGGGCAGAGGGCGGACGATCGCTCCACT

2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000
CGCCGGGACCAAGGTGCGGGGGCCCTGCCAGCCGCTGGGGCGTGGCCAGGCTCGAAGCACCCAGGTGTGCGGGGCCGACTCTAAGCCCTGGCACCGGAAGAGAGAGGGCGGGGATTGGA

3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120
CCTCCCGGCTCCAGCATTGCAACTGGGCGCTCCGTCTCCTGGTCCACGCAATGATGCTGCGGCTGCTCAGAAGCCAGGTAGCCTGCCCTGGGTGAAGCCTTCGCGCAGGTCAATGACGGG

3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240
GCGGAGGGGACAGGCGCGGTCCCTGCATCCCCGATCTGGGGAGCGGTGGGCCCAGGGGCCATCGCCTTAGCCCTGGCGTGGGGCTCGGCGCAAGTGACGGGCGGGGCTCCACCTTC

3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360
CAGCCATCCGCCCCGCGGGGAGGGCGGACGCTGGGAGACTCCCGGCCGCGCCCTCTCCTTCTCTCCTCCCAAGCCCTCGCTGCCAGTCCGGACAGGCTGCGCGGAGGGGAGGGGCTGC

3370 3380 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480
CGGGCGGATAGCCGGACGCTGGCGTTCCAGGGCGCGCGGATGTGCCTGCCTTTGCGGAGGTTGCGCTCCGGCCACGAAAGCGGACTGTGGATCTGCCACCTGCAAGCAGCTCGGG

3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600
TAAGTGGGACTGCCCACTCAGTTGTTCTGGGACCCAGGAACAACCTCTTCAGAACAGGAGGTGCACCCCCAACCTCTTCTCAGGTCTTCTAAGGCCCTAGGAATCTCGCCACC

Figure 3 (cont'd)

3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720
TCCCCAGCCATTACTCCTCCAGGAACCAAGATGCTCCTTCGGCTCCTGACCCTCCAGCCTCTCTTGTTTTACTTGAACATATCGTTTCCCATCACCACCTCTGTGGTGGATTTTGGCCTC

3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840
ACAGACAGGTACTCCTGAGAAACAGGCTGGTGAAGAGTCCAGTATCAGCGGAACCTACAGGAGGGGAGACTCGAGATTCTTCAGGAAAAGGTGTAGGAACCTGGACCACCTTTCTTTTTT

3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960
TTTTTTTTTTTTTTAAGACAGGGTCCCTCTCTGTGCGGCAAGCTGGAGTGCAGTCAGCGGTGCTATCGCGGCTCATTGTGAGCTCCGGGGATCCTCCCGCCTTAGCATCCGGTGTAG

3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080
CTGAGACCACAGACATGTGCCACCATGCCAAGCTAATTTATTTATTTTGGAGACGGAGTTTCACTCTTGTGCCCAGGCTGGAGTGTAAATGGCATGATCTCAGCTCACGCAAC

4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200
TCCCGCCCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTGGCTGGGATTACAGGCATGCGCCACCATGCCCGGCTAATTTGTATTTAAGTAGAGACAGGGTTTCTCCAGC

4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320
TTGGTCAGGCTGGTCTCGAACTCCCAACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGTGGGATTACAGGTGTGAGCCACCGCGCTGGCCCATGCCAAGCTAATTTAAATTT

4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440
TTTTGTAAAGAGTGTCTGTGCCCAGGCTGATCTGAACTCCTGGGTEAAGGGATCTECCATCTCAGCCTCCCAATATGCTGGGATTACAGGTGTGAGCCACAGTGGCCAGCCAAAC

4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560
CATGGCTATCTTGAAAACCACTTGTCTCCAGTCCCATGCCCGAAATTCGAAGGCTCTCATCCCTGAAACCTAGGACTCAGGCTCTCCCTACCTCAGCCCCAGGAGTCTAAACCTTTA

4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680
ACTTCCTCTTTCCCTGGGACTAAGGAGTGTGCACCCAGGCGCTCCCTTACCCACATCCCTCCTCAGCCTCCCTCCTCAGCCTCAGTGCATTTGCTAATTCGCTTTCCTCCCTG

4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800
CAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCTGCTAGTCTGTGCTCTCTGTAATCTTCTCTCCATATCCATCAAGACAGCTTTCCACATGGCCTAGGCCTGT
MetTrpLeuArgSerHisArgGlnLeuCysLeuAlaPheLeuLeuValCysValLeuSerValIlePhePheLeuHisIleHisGlnAspSerPheProHisGlyLeuGlyLeuS

4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920
CGATCCTGTGTCCAGACCGCGCTGGTGACACCCCAAGTGGCCATCTTCTGCCTGCCGGTACTGCGATGGGCCCCAACGCCTCCTCTCTGTCCCGAGCACCTGCTTCCCTCTCCG
erIleLeuCysProAspArgArgLeuValThrProProValAlaIlePheCysLeuProGlyThrAlaMetGlyProAsnAlaSerSerSerCysProGlnHisProAlaSerLeuSerG

4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040
GCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGATGCCACGCTGCTGGCTCTGCCCAGCTCAACGGCGCGCGGGCTTTATCCTGCCTGCCATGCATGCCG
lyThrTrpThrValTyrProAsnGlyArgPheGlyAsnGlnMetGlyGlnTyrAlaThrLeuLeuAlaLeuAlaGlnLeuAsnGlyArgArgAlaPheIleLeuProAlaMetHisAlaA

5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160
CCCTGGCCCGGTATTCCGCATCACCCTGCCGTGCTGGCCCCAGAGTGGACAGCCCGCAGCGGTGGCGGGAGCTGCAGCTTCACGACTGGATGTGCGAGGAGTACGCGGACTTGAGAG
laLeuAlaProValPheArgIleThrLeuProValLeuAlaProGluValAspSerArgThrProTrpArgGluLeuGlnLeuHisAspTrpMetSerGluGluTyrAlaAspLeuArgA

5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280
ATCCTTTCTGAAGCTCTCTGGCTTCCCTGCTCTTGGACTTTCTTCCACCATCTCCGGGAACAGATCCGAGAGAGTTACCCTGCAGGACACCTTCGGGAAGAGGCGCAGAGTGTGC
spProPheLeuLysLeuSerGlyPheProCysSerTrpThrPhePheHisHisLeuArgGluGlnIleArgArgGluPheThrLeuHisAspHisLeuArgGluGluAlaGlnSerValI

5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400
TGGGTCACTCCCGCTGGGCGCACAGGGGACCGCCCGCCACCTTTGTGGCGTCCACGTGCCCGTGGGGACTATCTGCAGGTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACA
euGlyGlnLeuArgLeuGlyArgThrGlyAspArgProArgThrPheValGlyValHisValArgArgGlyAspTyrLeuGlnValMetProGlnArgTrpLysGlyValValGlyAspS

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5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520
GCGCCTACCTCCGGCAGGCCATGGACTGGTTCGGGGCACGGCACGAAGCCCCCGTTTTCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCGATG
erAlaTyrLeuArgGlnAlaMetAspTrpPheArgAlaArgHisGluAlaProValPheValValThrSerAsnGlyMetGluTrpCysLysGluAsnIleAspThrSerGlnGlyAspV

5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640
TGACGTTTGGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAGTGC AACCAACCAATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCACCTGGCTG
alThrPheAlaGlyAspGlyGlnGluAlaThrProTrpLysAspPheAlaLeuLeuThrGlnCysAsnHisThrIleMetThrIleGlyThrPheGlyPheTrpAlaAlaTyrLeuAlaG

5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760
GCGGAGACACTGTCTACCTGGCCAACTTCACCTGCCAGACTCTGAGTTCCTGAAGATCTTTAAGCCGGAGGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAAATGCAGACTTGTCTCCAC
lyGlyAspThrValTyrLeuAlaAsnPheThrLeuProAspSerGluPheLeuLysIlePheLysProGluAlaAlaPheLeuProGluTrpValGlyIleAsnAlaAspLeuSerProL

5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880
TCTGGACATTGGCTAAGCCTTGAGAGCCAGGGAGACTTCTGAAGTAGCCTGATCTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCCTGGCATCTTCTGGAGAAGCTTGTGGTGTTC
euTrpThrLeuAlaLysProEnd

5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000
TGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGGGAGAGTTGGAGAGAAGGGGGACGTTTCTGGAACTGTCTGAATATTCTAGAACTAGCAAAACATCTTTTCTGATGGCTG

6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120
GCAGGCAGTTCTAGAAGCCACAGTGGCCACCTGCTCTTCCAGGCCATATCTACAGTACTTCCAGATGGCTGCCCCAGGAATGGGGAACCTCTCCCTCTGGTCTACTCTAGAAGAGGGGT

6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240
TACTTCTCCCTGGGTCTCCAAGACTGAAGGAGCATATGATTGCTCCAGAGCAAGCATTACCAAGTCCCTTCTGTGTTTCTGGAGTGATTCTAGAGGGAGACTTGTCTAGAGAGG

6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360
ACCAGGTTTGATGCCTGTGAAGAACCTGCAGGGCCCTTATGGACAGGATGGGGTCTGGAAATCCAGATAACTAAGGTGAAGAATCTTTTAGTTTTTTTTTTTTTTTTTGGAGACAG

6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480
GGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGTGATCTTGGTCACTGCAACTTCCGCCTCCTGTGTTCAAGCGATTCTCCTGTCTCAGCCTCCTGAGTAGATGGGACTACAGGC

6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600
ACAGGCCATTATGCCTGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTACCATGTTGGCCGGGATGGTCTCGATCTCCTGACCTTGTCATCCACCTGTCTTGGCCTCCCAAAGTGC

6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720
TGGGATTACTGGCATGAGCCACTGTGCCAGCCCGGATATTTTTTTTAATTATTTATTTATTTATTTATTTATTTAGACGGAGTCTTGCTCTGTAGCCAGGCCAGAGTGCAGTGGCGC

6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840
GATCTCAGETCACTGCAAGCTCTGCCTCCCGGGTTCATGCCATTCTGCCTCAGCCTCCTGAGTAGCTGGGACTACAGGCGCCCGCCACCACGCGCCGGCTAATTTTTTTGTATTTTAGT

6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960
AGAGACGGGGTTTCATCGTGTTAACCAAGATGGTCTCGATCTCCTGACCTCGTGATCTGCCACCTCGGCCTCCACAGTGCTGGGATTACCGGGCTGAGCCACCATGCCTGGCCCGGA1

6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080
AATTTTTTTTAATTTTTGTAGAGACGAGGTCTTGTGATATTGCCAGGCTGTCTTCAACTCCTGGGCTCAAGCAGTCTCCACCTTGGCCTCCCAAGATGCTGGGTTTATAGATGTG/

7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200
GCCAGCACACCGGGGCCAAGTGAAGAATCTAATGAATGTGCAACCTAATTGTAGCATCTAATGAATGTTCACCATTTGCTGGAAAAATTGAGATGGAAAAACAAACCATCTCTAGTTGGCC

[illegible]

[illegible]

910	920	930	940	950	960
CCTTG ACGAC AAGGG CCTTC GGGGG GGCCA CATCT TCATC TTTGG TTTAT GAGTC CTGTG					
970	980	990	1000	1010	1020
CGTCT TGGTA CAAGC AATAC TACTA TGAGC CGGCA AGTCA GACTT ATTTC GTAGG GGACC					
1030	1040	1050	1060	1070	1080
AAAGG AAAGA ACATG TTTTG ATTGC TAAGA AAACA TTTTG TTCTC TATCC TTTAC TGGGC					
1090	1100	1110	1120	1130	1140
TGGCA GGCAG AGGAA ATGTT CTTAT GAGCA CTCAC ATTGA AAACG TAAGT TCTTC ACCAA					
1150	1160	1170	1180	1190	1200
ATGCA GAGAC TGTGA AGGCC AGGCC GGTGC GGGCT GCGTC GACAA TGGGA GCGTC TCGGC					
1210	1220	1230	1240	1250	1260
GGGCC AGGAG ATGCT GGGCA GGGAT GGGGT GGGCG GCGCT CTGCT GCGAC GTTCC CCCGG					
1270	1280	1290	1300	1310	1320
CCTCT GGAAT GCGTC GGTCC GTCAA TGGCT GCGTC GGGCG GGGGT GCGTC GCGGC TGGCT					
1330	1340	1350	1360	1370	1380
AGGCC CAACG GCGAG AAGCC GACGC TATCC TCGCT TCGCG GCGCG GGGGT CCGCC TTCCG					
1390	1400	1410	1420	1430	1440
TCTGT TCTAG GGGCT GGTCC TGGCG GGCAG CTGCT TTAGA AGGTC TCGAG CCTCC TGTAC					
1450	1460	1470	1480	1490	1500
CTTCC CAGGG ATGAA CCGGG CCTTC CCTCT GGAAG GCGAG GGTTC GGGCC ACAGT GAGCG					
1510	1520	1530	1540	1550	1560
AGGGC CAGGG CCGTG GCGCG GCGCA GAGGG AAACC GGATC AGTTG AGAGA GAATC AAGAG					
1570	1580	1590	1600	1610	1620
TAGCG GATGA GCGCG TTGTG GGGCG GGGCC GGGAA GCGCT GGGGC GCGGG CTGGG AGAAG					
1630	1640	1650	1660	1670	1680
GAGTG GCGCG AGGCG CCGCA GGAGG CTCCC GGGGC CTGGT GGGGC GGGCT GGGCC CCGGG					
1690	1700	1710	1720	1730	1740
CGCAG TGGAA GAAAG GGACG GCGCG TGCCC GGTTC GCGCT CCGTC CCAGC TCACC TTGCC					
1750	1760	1770	1780	1790	1800
CTGGC GCGTC GCGCC GCGCG GCACT TGGGA GGAGC AGGGC AGGGC GCGCG GCGCT TGCAT					

[illegible]

1810 1820 1830 1840 1850 1860
TCTGG GACCG CCCCC TTCCA TTCCC GGGCC AGCGG CGAGC GGCAG CGACG GCTGG AGCCC
1870 1880 1890 1900 1910 1920
CAGCT ACAGC ATGAG AGCCG GTGCC GCTCC TCCAC GCCTG CGGAC GCGTG GCGAG CGGAG
1930 1940 1950 1960 1970
GCAGC GCTGC CTGTT CGCGC C ATG GGG GCA CCG TGG GGC TCG CCG ACG GCG GCG
Met Gly Ala Pro Trp Gly Ser Pro Thr Ala Ala
1980 1990 2000 2010 2020
GCG GGC GGG CGS CSC GSG TGG CGC CGA GGC CGG GGG CTG CCA TGG ACC GTC TGT
Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Trp Thr Val Cys
2030 2040 2050 2060 2070 2080
GTG CTS GCG GCG CSC GSG TTS ACG TGT ACG GCG CTG ATC ACC TAC GCT TSC TGG
Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp
2090 2100 2110 2120 2130
GGG CAG CTG CCG CSC CTG CSC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC
Gly Gln Leu Pro Pro Leu Pro Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly
2140 2150 2160 2170 2180 2190
GTG CTG CTG TGG TGG GAG CSC TTC GGG GGG CGC GAT AGC GCC CCG AGG CCG CCC
Val Leu Leu Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro
2200 2210 2220 2230 2240
CCT GAC TCC CCG CTS CGC TTC AAC ATC AGC GGC TGC CGC CTG CTC ACC GAC CGC
Pro Asp Cys Pro Leu Arg Phe Asn Ile Ser Gly Cys Arg Leu Leu Thr Asp Arg
2250 2260 2270 2280 2290
GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CAC CGC GAC CTC GTG AAG
Ala Ser Tyr Gly Glu Ala Gln Ala Val Leu Phe His His Arg Asp Leu Val Lys
2300 2310 2320 2330 2340 2350
GGG CCC CCC GAC TGG CCC CCG CCC TGG GGC ATC CAG GCG CAC ACT GCC GAG GAG
Gly Pro Pro Asp Trp Pro Pro Pro Trp Gly Ile Gln Ala His Thr Ala Glu Glu
2360 2370 2380 2390 2400
GTG GAT CTG CGC GTG TTG GAC TAC GAG GAG GCA GCG GCG GCG GCA GAA GCC CTG
Val Asp Leu Arg Val Leu Asp Tyr Glu Glu Ala Ala Ala Ala Ala Glu Ala Leu
2410 2420 2430 2440 2450 2460
GCG ACC TCC AGC CCC AGG CCC CCG GGC CAG CSC TGG GTT TGG ATG AAC TTC GAG
Ala Thr Ser Ser Pro Arg Pro Pro Gly Gln Arg Trp Val Trp Met Asn Phe Glu
2470 2480 2490 2500 2510
TCG CCC TCG CAC TCC CCG GGG CTG CGA AGC CTG GCA AGT AAC CTC TTC AAC TGG
Ser Pro Ser His Ser Pro Gly Leu Arg Ser Leu Ala Ser Asn Leu Phe Asn Trp

2030

[illegible]

2520 2530 2540 2550 2560
ACG CTC TCC TAC CGG GCG GAC TCG GAC GTC TTT GTG CCT TAT GGC TAC CTC TAC
Thr Leu Ser Tyr Arg Ala Asp Ser Asp Val Phe Val Pro Tyr Gly Tyr Leu Tyr

2570 2580 2590 2600 2610 2620
CCC AGA AGC CAC CCC GCG GAC CCG CCC TCA GGC CTG GCC CCG CCA CTG TCC AGG
Pro Arg Ser His Pro Gly Asp Pro Pro Ser Gly Leu Ala Pro Pro Leu Ser Arg

2630 2640 2650 2660 2670
AAA CAG GGG CTC GTG GCA TGG GTG GTG AGC CAC TGG GAC GAG CGC CAG GCC CGG
Lys Gln Gly Leu Val Ala Trp Val Val Ser His Trp Asp Glu Arg Gln Ala Arg

2680 2690 2700 2710 2720 2730
GTC GGC TAC TAC CAC CAA CTC AGC CAA CAT GTG ACC GTG GAC GTG TTC GGC CGG
Val Arg Tyr Tyr His Gln Leu Ser Gln His Val Thr Val Asp Val Phe Gly Arg

2740 2750 2760 2770 2780
GGC GGG CCG GGG CAG CCG GTG CCC GAA ATT GGG CTC CTG CAC ACA GTG GCC CGC
Gly Gly Pro Gly Gln Pro Val Pro Glu Ile Gly Leu Leu His Thr Val Ala Arg

2790 2800 2810 2820 2830
TAC AAG TTC TAC CTC GGT TTC GAG AAC TCG CAG CAC CTC GAT TAT ATC ACC GAG
Tyr Lys Phe Tyr Leu Ala Phe Glu Asn Ser Gln His Leu Asp Tyr Ile Thr Glu

2840 2850 2860 2870 2880 2890
AAG CTC TGG CGC AAC GCG TTG CTC GGT GGG GCG GTG CCG GTG GTG CTC GGC CCA
Lys Leu Trp Arg Asn Ala Leu Leu Ala Gly Ala Val Pro Val Val Leu Gly Pro

2900 2910 2920 2930 2940
GAC GGT GCG AAC TAC GAG GCG TTT GTG GCG GCG GGC GCC TTC ATC CAC GTG GAC
Asp Arg Ala Asn Tyr Glu Arg Phe Val Pro Arg Gly Ala Phe Ile His Val Asp

2950 2960 2970 2980 2990 3000
GAC TTC CCA AGT GCC TCC TCC CTG GCC TCG TAC CTG CTT TTC CTC GAC CGC AAC
Asp Phe Pro Ser Ala Ser Ser Leu Ala Ser Tyr Leu Leu Phe Leu Asp Arg Asn

3010 3020 3030 3040 3050
CCC GCG GTC TAT CGC CGC TAC TTC CAC TGG CGC CGG AGC TAC GCT GTC CAC ATC
Pro Ala Val Tyr Arg Arg Tyr Phe His Trp Arg Arg Ser Tyr Ala Val His Ile

3060 3070 3080 3090 3100
ACC TCC TTC TGG GAC GAG CCT TGG TGC GCG GTG TCC CAG GCT GTA CAG AGG GCT
Thr Ser Phe Trp Asp Glu Pro Trp Cys Arg Val Cys Gln Ala Val Gln Arg Ala

3110 3120 3130 3140 3150 3160
GGG GAC GCG CCC AAG AGC ATA GCG AAC TTG GCG AGC TGG TTC GAG GCG TGA A
Gly Asp Arg Pro Lys Ser Ile Arg Asn Leu Ala Ser Trp Phe Glu Arg ***

[illegible][illegible]

Figure 7 (page 1)

α(1,3)FT DNA (-128)	TTTTTCTCA
α(1,3)FT DNA (-120)	TCTGTGAACACAGGAATAAACAGCTCTTCTCAGGACTCATGGCCCTGGAGCTTTGGTAAG
α(1,3)FT DNA (-60)	CAGGAGATTGTCATCAATGACCTCACTCTCTCTCTCCCCACTTCCCAGAGACTCTGACCC
α(1,3)FT AA	M D P L G P A K P Q W S W R C C L T T L
α(1,3)FT DNA (1)	ATGGATCCCCCTGGGCCCCGCCAAGCCACAGTGGTGGCGCTGCTGTCGACCCACGCTG
Lewis FT DNA	
	ATGGATCCCCCTGGGTGCAGCCCAAGCCACAATGGCCATGGCGCGCTGTCTGGCGGCACTG
α(1,3)FT AA	L F Q L L M A V C F F S Y L R V S Q D D
α(1,3)FT DNA (61)	CTGTTTCAGCTGCTGATGGCTGTGTGTTTCTTCTCTATCTGCGTGTGTCTCAAGACGAT
Lewis FT DNA	
	CTATTTTCAGCTGCTGTTGGCTGTGTGTTTCTTCTCTACCTGCGTGTGTCTCCCGAGACGAT
α(1,3)FT AA	→ P T V Y P N G S R F P D S T G T P A H S
α(1,3)FT DNA (121)	CCCACTGTGTACCCCTAATGGGTCC...CGCTTCCCA..GACAGCACAGGGACCCCGCCCACTCC
Lewis FT DNA	
	GCCACTGGATCCCCCTAG.GGCTCCCAGTGGGTCTCCCGACAGGACACC.ACTCCACCCGCCCC
α(1,3)FT AA	I P L I L L W T W P F N K P I A L P R C
α(1,3)FT DNA (181)	ATCCCCCTGATCCTGTGTGGACGTGGCCTTTTAAACAACCCATAGCTCTGCCCGCTGC
Lewis FT DNA	
	ACCCCTCTGATCCTGTATGGACATGGCCTTTCCACATCCCTGTGGCTCTGTCCCGCTGT
α(1,3)FT AA	S E M V P G T A D C N I T A D R K V Y P
α(1,3)FT DNA (241)	TCAGAGATGTGCTGGCAGCGCTGACTGCAACATCACTGCCGACCGCAAGGTGTATCCA
Lewis FT DNA	
	TCAGAGATGTGCTGGCGGCACAGCCGACTGCCACATCACTGCCGACCGCAAGGTGTATCCA

Figure 7 (page 2)

α(1,3)FT AA	Q A D A V I V H H R E V M Y N P S A Q L
α(1,3)FT DNA (301)	CAGGCAGACGGGTCTCGTGCACACCGAGAGGTATGTACAAACCCAGTGCACGCTC
Lewis FT DNA	
	CAGGCAGACACGGTCTCGTGCACACCGAGAGGTATGTATCCAAACCTAAGTCACGCTC
α(1,3)FT AA	P R S P R R Q G Q R W I W F S M E S P S
α(1,3)FT DNA (361)	CCACGCTCCCCGAGGGCGAGGGCGAGCGATGGATCTGGTTCAGCAGTGGAGTCCCCAAGC
Lewis FT DNA	
	CCACCTTCCCCGAGGGCGAGGGCGAGCGTGGATCTGGTTCAACTTGGAGCCACCCCT
α(1,3)FT AA	H C W Q L K A M D G Y F N L T M S Y R S
α(1,3)FT DNA (421)	CACTGCTGGCAGCTGAAGCCATGGACGGATACTTCAATCTCACCATGTCTCCTACCGCAGC
Lewis FT DNA	
	AACTGCCAGCACCTGGAAGCCCTGGACAGATACTTCAATCTCACCATGTCTCCTACCGCAGC
α(1,3)FT AA	D S D I F T P Y G W L E P W S G Q P A H
α(1,3)FT DNA (481)	GACTCCGACATCTTCACGCCCTACGGCTGGCTGGAGCCGTGGTCCGGCCAGCCTGCCAC
Lewis FT DNA	
	GACTCCGACATCTTCACGCCCTACGGCTGGCTGGAGCCGTGGTCCGGCCAGCCTGCCAC
α(1,3)FT AA	P P L N L S A K T E L V A W A V S N W G
α(1,3)FT DNA (541)	CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCCCTGGGCAGTGTCCAACTGGGGG
Lewis FT DNA	
	CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCCCTGGGCAGTGTCCAACTGGGAG
α(1,3)FT AA	P N S A R V R Y Y Q S L Q A H L K V D V
α(1,3)FT DNA (601)	CCAAACTCCGCCAGGTGCGCTACTACAGAGCCTGCAGGCCCATCTCAAGGTGGACGTG
Lewis FT DNA	
	CCGGACTCAGCCAGGTGCGCTACTACAGAGCCTGCAGGCTCATCTCAAGGTGGACGTG

Figure 7 (page 3)

$\alpha(1,3)$ FT AA	Y G R S H K P L P Q G T M M E T L S R Y
$\alpha(1,3)$ FT DNA (661)	TACGGACGCTCCCAAGCCCTGCCCCAGGGAACCATGATGGAGACGCTGTCCCGGTAC
Lewis FT DNA	
$\alpha(1,3)$ FT AA	K F Y L A F E N S L H P D Y I T E K L W
$\alpha(1,3)$ FT DNA (721)	AAGTTCTATCTGGCCTTCGAGAACTCCTTGACCCCGACTACATCACCAGAAAGCTGTGG
Lewis FT DNA	
$\alpha(1,3)$ FT AA	R N A L E A W A V P V L G P S R S N Y
$\alpha(1,3)$ FT DNA (781)	AGGAACGCCCTGGAGGCCCTGGGCCGTGCTGGGCCCCAGCAGAAAGCAACTAC
Lewis FT DNA	
$\alpha(1,3)$ FT AA	E R F L P P D A F I H V D D F Q S P K D
$\alpha(1,3)$ FT DNA (841)	GAGAGGTTCTGCCACCCGACGCCCTTCATCCACGTGGACGACTTCCAGAGCCCCAAGGAC
Lewis FT DNA	
$\alpha(1,3)$ FT AA	L A R Y L Q E L D K D H A R Y L S Y F R
$\alpha(1,3)$ FT DNA (901)	CTGGCCCCGTACCTGCAGGAGCTGGACAAGGACCACGCCCGCTACCTGAGCTACTTTCGC
Lewis FT DNA	
$\alpha(1,3)$ FT AA	W R E T L R P R S F S W A L A F C K A C
$\alpha(1,3)$ FT DNA (961)	TGGCGGGAGACGCTGGGCCCTCGCTCCTTCAGCTGGGCACTCGCTTCTGCAAGGCCCTGC
Lewis FT DNA	
$\alpha(1,3)$ FT AA	W K L Q E E S R Y Q T R G I A A W F T Stop
$\alpha(1,3)$ FT DNA (1021)	TGGAAACTGCAGGAGGAATCCAGGTACCAGACACGGGC...ATAGCGCTTGGTTCACCTGA
Lewis FT DNA	

Figure 7 (page 4)

GAGGCTGGTGTGGGGCCCTGGGCTGCCAGGAACCTCATTTTCCTGGGGCCCTCACCTGAGTG
GGGGCCCTCATCTACCTAAGGACTCGTTTGCCTGAAGCTTCACCTGCCTGAGGACTCACCT
GCCTGGGACGGTCACCTGTTGCAGCTTCACCTGCCCTGGGATTACCTACCTGGGTCTC
ACTTTCCTGGGGCCCTCACCTGCTGGAGTCTTCGGTGGCCAGGTATGTCCTTACCTGGGA
TTTCACATGCTGGCTTCCAGGAGCGTCCCCCTGCCGAGCCCTGGCCCTGCTGGGGATGCTC
CTGGGGACTTTGCCCTACTGGGGACCTCGGCTGTTGGGGACTTTACCTGCTGGGGACCTGCT
CCCAGAGACCTTCCACACTGAATCTCACCTGCTAGGAGCCTCACCTGCTGGGGACCTCAC
CCTGGAGGCACTGGGGCCCTGGGAACT

Figure 8.

